

coding region of the gene are eliminated,

and

(B) sequences encoded by AATAAA, NATAAA, ANTAAA, AANAAA, AATNAA, AATANA, or AATAAN within the coding region of the gene are eliminated.

47. The method of making the nucleic acid according to claim 46, wherein the gene is derived from yeast.

48. The method of making the nucleic acid according to claim 46, wherein the gene derived from yeast is a ferric-chelate reductase gene.

49. The method of making the nucleic acid according to claim 46, wherein codon usage of the base sequence is modified to increase a preferred codon of the plant.


D<sup>9</sup>  
50. The method of making the nucleic acid according to claim 46, wherein there is no observable difference in content between base G and base C throughout the gene to be introduced.

51. The method of making the nucleic acid according to claim 46, wherein the base sequence is optimized such that ATTTA sequences are eliminated, without altering the amino acid sequence.

52. The method of making the nucleic acid according to claim 46, wherein the base sequence located upstream of the gene's initiation codon is altered to a sequence for effective translation of mRNA known as Kozak sequence.

53. The method of making the nucleic acid according to claim 46, wherein the nucleic acid is DNA.

54. The method of making the nucleic acid according to claim 53, wherein the DNA has a base sequence as set forth in SEQ ID NO: 1.

 ~~55.~~ A nucleic acid having a modified base sequence of a ferric-chelate reductase gene derived from *Saccharomyces cerevisiae* FRE1, wherein the sequence is modified by features (A) and (B) without altering the amino acid sequence thereof, for eliminating the sequences relating to poly(A) addition, and for introducing said gene into a plant,

wherein features (A) and (B) are defined as follows:

(A) GT rich regions comprising 8 or more consecutive bases of G or T are eliminated,

and

(B) sequences encoded by AATAAA, NATAAA, ANTAAA, AANAAA, AATNAA, AATANA, or AATAAN are eliminated.

56. The DNA according to claim 55, wherein the DNA has a base sequence as set forth in SEQ ID NO: 1.

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#### IN THE DRAWINGS:

Kindly replace drawing sheets 1/18 – 18/18 with the enclosed substitute drawing sheets 1/19 – 19/19.

#### REMARKS

Claims 30-45 have been cancelled and new claims 46-56 have been added. The specification has been amended merely to comply with the sequence rules. Suitable formal drawings (19 sheets) are also submitted as a matter of formality. No new matter has been added by virtue of these amendments; support therefore being found throughout the specification and in the original claims of the application. In particular, support for the newly proposed claims appears in the present application at page 5, lines 5-14, page 8, lines 8-15 and lines 21-24, page 14, lines 2-10, and page 20, lines 6-13.